



# DNA Endogamy Research

Tanner Tolman, AG®  
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## Common Endogamous Groups

- Jews
- Polynesians
- Low German Mennonites
- The Amish
- French Canadians
- Arabic countries
- Newfoundlanders
- Islanders
- Early Colonial American populations
- Acadians

## Problems with Endogamy

### The Leeds Method

The Leeds is a commonly used method to sort your matches into four distinct clusters, one from each grandparent. While it is a great method for many people, it assumes that your four grandparents were not related to each other. If two or more of your grandparents were related through endogamy then this method becomes much more difficult to use if not impossible. For more information about the Leeds method click here (<https://www.danaleeds.com/the-leeds-method>).

### The Shared Centimorgan Project

The shared centimorgan (cM) project predicts the relationship between two people based on the amount of DNA that they share. For people with endogamy, the true relationship is going to be farther back than what the shared cM project predicts. To access the project click here (<https://dnapainter.com/tools/sharedcmv4>).

## Ways Around Endogamy

### Are Your Parents Related?

If your parents are related to each other, you can upload your DNA data into GEDmatch.com and use their "Are your parents related?" tool. The tool searches for homozygous regions of your DNA. In other words it looks to see if there are any places where your maternal and

paternal chromosomes are identical. If it finds any, then your parents must descend from a common ancestor who is the source of that DNA in both of them.

A good way to estimate how closely your parents are related is to multiply the amount of similar DNA by 4. If they are distantly related through endogamy there will likely be several small segments (0-15 cM's). If they have larger segments, they are likely related more closely.

One of the best ways to get around endogamy is through chromosome mapping. Before starting your chromosome mapping you will first want to identify all of these homozygous segments in your own DNA. Relatives who match you in those spots could be related to either one of your parents.

## **Y-DNA and mtDNA**

Y-DNA and mtDNA are immune to endogamy. The problem with endogamy is that people are distantly related through many lines. Y-DNA and mtDNA only examine your direct paternal and direct maternal lines.

## **Test Everyone**

This is good advice regardless of whether you have endogamy or not, but if you do have endogamy, then this is especially important. Test everyone in the oldest living generation that you can. Test your parents, grandparents, and great grandparents if you are lucky enough for them to still be living. Autosomal DNA becomes harder and harder to use the more generations removed a test taker is from the research problem. After only about 6 generations it is extremely difficult to solve problems. If any of them have siblings who are still living test them to. They will have some genes that they inherited from their parents that your direct ancestors did not. Once someone dies, the opportunity to obtain their DNA is gone, but if you invest in sending them a test now, you can use it for the rest of your life. Testing the oldest living generation will provide greater clarity to help sort out who is related closely and who is only a distant relative through endogamy.

I have followed my own advice and tested everyone I can. I have bought DNA tests for many people who have since passed away. Even though they are gone, their DNA results are not. I continue to use their DNA for my own research and my research is infinitely easier now as a result.

## **Chromosome Mapping**

Besides Y-DNA and mtDNA most of the tools to get around chromosome mapping involve chromosome mapping. I recommend you start this process in DNA painter (<https://dnainter.com>). Chromosome mapping creates a custom map of your DNA and shows which segments were inherited from each ancestor. They take time to make, but greatly speed up your research once they are built. You can overlay the DNA segments you share with a match onto your map to see who the common ancestor is. To do this, you will need access to a

chromosome browser. All of the DNA companies offer one except Ancestry and Living DNA. If you tested with one of them, you can download your raw data to FamilyTreeDNA.com, GEDmatch.com, or MyHeritage.com and use their chromosome browser.

Visual phasing is a process that compares the DNA of siblings to determine which segments came from each of your four grandparents. I recommend that you use visual phasing to create chromosome maps for the oldest living generation if possible. If you suspect you have endogamy, use GEDmatch's Are your parents related tool on all the siblings and see where the homozygous segments appear in each one. Proceed but with caution at those points. Relatives who match the siblings in those spots could be related on either side.

As you are chromosome mapping you will often find that segments from a man and woman who married or at least had a child together will end up right next to each other, but they will never overlap. One will start and right when the other stops on your map and vice versa. Be careful with this. Adjacent segments it is not proof that two ancestors were married and many segments will be next to each other by coincidence. (Each segment after all needs to be adjacent to another unless it fills the entire chromosome).

## **Segment Size**

Endogamy increases the amount of DNA that two people share, but it does not affect the size of those segments. People related only distantly through endogamy will likely share many small segments (0-19 cM's) scattered throughout. If larger segments are present, then that suggests a closer relationship between the two people. A chromosome browser shows exactly which segments are which. Ancestry DNA offers clues to help you determine this information as well even though they do not offer a chromosome browser. Clicking on a match will tell you how big the largest segment is, the total amount of DNA shared, and the total number of segments. You thus know how big the largest segment is and can calculate the average segment size of the remaining segments. This will help determine if you are related more closely to a match or likely just through distant endogamy.

The reason larger segments tend to be shared with closer relatives is because a centimorgan represents the odds that a segment will be split in half and only half of it given to the next generation. One centimorgan = a 1% chance. A 100 cM segment will be split one time on average in the next generation.